AMENDMENT OF THE CLAIMS

Please amend the claims as follows. This listing of claims will replace all prior versions and listings of claims in the application.

1. (Currently amended) A method for determining whether a human immunodeficiency virus type 1 (HIV-1) has an increased likelihood of having a reduced susceptibility to treatment with amprenavir, comprising: detecting whether the protease encoded by said HIV-1 exhibits the presence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at amino acid position 11, 34, 47, ~~48,~~ 50, 76, 83, 91 or 95 of an amino acid sequence of said protease, wherein the mutation at amino acid position 34 is Q, ~~the mutation at amino acid position 43 is T,~~ and wherein the presence of said mutation indicates that the HIV- 1 has an increased likelihood of having reduced susceptibility to treatment with amprenavir, with the proviso that said mutation is not ~~V32I,~~ I47V, or I50V, and wherein the level of susceptibility, mutations, and position number are ~~compare~~ compared to the protease sequence of the NL4-3 reference strain.

Claims 2-11 (Canceled)

12. (Currently amended) The method of claim 1, wherein the amino acid at position 11, ~~48,~~ 76, 91 or 95 of said protease is an amino acid having a neutral, hydrophobic or non-polar side chain.

13. (Original) The method of claim 12, wherein the amino acid at position 11 of said protease is I or L.

Claims 14-20 (Canceled)

21. (Original) The method of claim 12, wherein the amino acid at position 76 of said protease is V.

Claims 22-23 (Canceled)

24. (Original) The method of claim 12, wherein the amino acid at position 91 of said protease is A or V.

25. (Original) The method of claim 12, wherein the amino acid at position 95 of said protease is F.

Claims 26-28 (Canceled)

29. (Previously presented) The method of claim 1, wherein the amino acid at position 83 of said protease is an amino acid with an acidic, hydrophilic or polar side chain.

30. (Canceled)

31. (Original) The method of claim 1, wherein the amino acid at position 83 of said protease is D.

Claims 32-38 (Canceled)

39. (Original) The method of claim 1, wherein the amino acid at position 91 of said protease is an amino acid with a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.

40. (Original) The method of claim 1, wherein the amino acid at position 91 of said protease is an amino acid with a neutral, hydrophilic or polar side chain.

41. (Original) The method of claim 40, wherein the amino acid at position 91 of said protease is S.

42. (Currently amended) The method of claim 1, wherein the method comprises detecting the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at least 2, 3, 4, 5, 6, 7, or 8, ~~9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19~~ of the amino acid positions.

43. (New) The method of claim 1, further comprising detecting at least one of a mutation of an amino acid at 32, 33, 43, 46, 48, 54, 58, 71, 79, 82, or 84 wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having reduced susceptibility to treatment with amprenavir, with the proviso that the mutation is not V32I, M46I, M46L, I54L, I54M, or I84V, and wherein the level of susceptibility, mutations, and position number are compare to the protease sequence of the NL4-3 reference strain.

44. (New) The method of claim 43, wherein the amino acid at position 33, 43, 48, 54, 71, 82 or 84 of said protease is an amino acid having a neutral, hydrophobic or non-polar side chain.

45. (New) The method of claim 44, wherein the amino acid at position 33 of said protease is F.

46. (New) The method of claim 44, wherein the amino acid at position 48 of said protease is M.

47. (New) The method of claim 44, wherein the amino acid at position 54 of said protease is A.

48. (New) The method of claim 44, wherein the amino acid at position 71 of said protease is L.

49. (New) The method of claim 44, wherein the amino acid at position 82 of said protease is A or F.

50. (New) The method of claim 44, wherein the amino acid at position 84 of said protease is A.

51. (New) The method of claim 44, wherein the amino acid at position 43 of said protease is T.

52. (New) The method of claim 43, wherein the amino acid at position 54 of said protease is an amino acid having a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.

53. (New) The method of claim 52, wherein the amino acid at position 54 of said protease is S or T.

54. (New) The method of claim 43, wherein the amino acid at position 58 of said protease is an amino acid having an acidic, hydrophilic or polar side chain.

55. (New) The method of claim 54, wherein the amino acid at position 58 of said protease is E.

56. (New) The method of claim 43, wherein the amino acid at position 79 of said protease is an amino acid having a neutral, hydrophobic, non-polar, acidic, hydrophilic or polar side chain.

57. (New) The method of claim 56, wherein the amino acid at position 79 of said protease is not P.

58. (New) The method of claim 43, wherein the amino acid at position 84 of said protease is an amino acid having a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.

59. (New) The method of claim 58, wherein the amino acid at position 84 of said protease is C.

60. (New) The method of claim 43, wherein the method comprises detecting the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 of the amino acid positions.